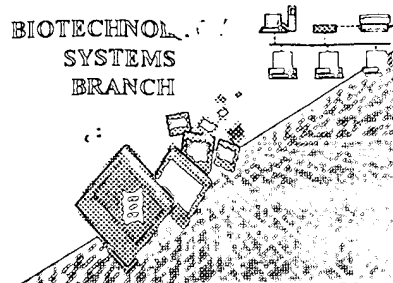


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/842,930

Source: OIPK

Date Processed by STIC: 5/11/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORRED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/842930

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 8 _____ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 _____ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of "Artificial" (NEW RULES) Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.
- 12 _____ Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 _____ PatentIn ver. 2.0 "bug" **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/842,930

DATE: 05/11/2001
TIME: 15:27:41

Input Set : A:\SEQUENCES.txt
Output Set: N:\CRF3\05112001\I842930.raw

Does Not Comply
Corrected Diskette Needed
pr 1-5

4 <110> APPLICANT: Weigel et al.
W--> 5 <120> TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
W--> 6 <130> FILE REFERENCE: 5820.603
W--> 7 <140> CURRENT APPLICATION NUMBER: Not Yet Assigned
C--> 8 <141> CURRENT FILING DATE: 2001-04-25
E--> 9 <160> NUMBER OF SEQ ID: 57
10 <170> SOFTWARE: WordPerfect 8.0 *Software*

ERRORED SEQUENCES

W--> 11 <210> SEQ ID NO: 1
12 <211> LENGTH: 4706
13 <212> TYPE: DNA
14 <213> ORGANISM: Rattus Norvegicus
W--> 15 <220> FEATURE:
E--> 16 <400> SEQUENCE: 0
C--> 19

21
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*see p. 2
for explanation*

tctttaccaa gtctactcac ccgtctggag ca
tacattattc attacaacct ggcaagtgc a
gtgccaaaca atgaagccat cgaaaactat at
gaagatattc tacggtacca tgtggtcctg gg
aacggcatgc accgagagac catgctgggg tt
aatgaccagc tgtatgtaaa tgaagctcca at
ggagtgatcc atgggtctgga gaaagttctg ga
gacaccatta ttgtgagagg ggagtgtgga aa
gagacaaaac cacttagaga gacgaggaaa tg
agatccgtat tcatcgggtg ccagccacag tg
tggttggtctt ctttggccca caatgccaa g
ctgggaacgg cttctgtctg ggacggtgtg aa
ggcttcaatg ggacagcctg tgaaacctgc ac
caagcatgct cttgtgtcca tgggagatgt ag
gactgtgacg tcggctggcg aggagtgaag tg
aacgggacct gtcacaccag tgccaactgc ct
aaatgtgcgg caggattccg agggaaatgga ac
accagcaatg gaggatgttc taaaaggcc ga
gtgtgtgtgt gcaaggcagg ctataccggc ga

~~delete~~
~~SEQUENCE LISTING~~

<110> Weigel et al.
 <120> Identification of Hyaluronan Receptor for Endocytosis
 <130> 5820.603
 <140> Not Yet Assigned
 <141> Herewith
 <160> 57
 <170> WordPerfect 8.0 *Software*
 <210> 1
 <211> 4706
 <212> DNA
 <213> Rattus Norvegicus
 <220>

<223> <400> HARE CDNA

<400> 1 ← This mandatory numeric identifier and response appears before each sequence

GTCTACTCAC CCGTCTGGAG CAGATGCCCCG ACTATTCCAT TTTCCGAGGT	60
ATTACAACCT GGCAAGTGCA ATCGAGTCTG CAGATGCTTA TACTGTGTTC	120
ATGAAGCCAT CGAAAACTAT ATCAGGGAGA AGAAAGCCAC ATCTCTAAAG	180
TACGGTACCA TGTGGTCCTG GGGGAAAAGC TCCTGAAGAA TGAATTGCAT	240
ACCGAGAGAC CATGCTGGGG TTCTCCTACC TCCTTGCCTT CTTTCTCCGC	300

TCTTTACCAA

TACATTATTC

GTGCCAAACA

GAAGATATTC

AACGGCATGC

Per 1.822 of Sequence Rules, group all non-coding bases into 10's on same line, with cumulative base total figure at right margin of each line.
 60 bases per line - all bases must be in lower-case letters when in new Sequence Rules format.

Please follow this format for all nucleic acid sequences throughout Sequence Listing.

9/842,930 3

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/842,930

DATE: 05/11/2001
TIME: 15:27:41

Input Set : A:\SEQUENCES.txt
Output Set: N:\CRF3\05112001\I842930.raw

W--> 195 <110> APPLICANT: Weigel et al.
W--> 195 <110> APPLICANT: Weigel et al.
W--> 196 <120> TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
W--> 196 <120> TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
W--> 196 <120> TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
W--> 197 <130> FILE REFERENCE: 5820.603
W--> 197 <130> FILE REFERENCE: 5820.603
W--> 197 <130> FILE REFERENCE: 5820.603
W--> 198 <140> CURRENT APPLICATION NUMBER: Not Yet Assigned
199 <141> CURRENT FILING DATE: Herewith
W--> 200 <160> NUMBER OF SEQ ID: 57
W--> 200 <160> NUMBER OF SEQ ID NOS: 57
W--> 200 <160> NUMBER OF SEQ ID NOS: 57
W--> 201 <170> SOFTWARE: WordPerfect 8.0 *Software*
W--> 202 <210> SEQ ID NO: 2
203 <211> LENGTH: 1431
204 <212> TYPE: PRT
205 <213> ORGANISM: Rattus norvegicus
W--> 206 <220> FEATURE:
E--> 207 <400> SEQUENCE: 0
E--> 211 Ser Leu Pro Ser Leu Leu Thr Arg Leu Glu Gln Met Pro Asp Tyr Ser Iso Phe Arg
212 1 5 10 15
E--> 214 Gly Tyr Iso Iso His Tyr Asn Leu Ala Ser Ala Iso Glu Ser Ala Asp Ala Tyr Thr
215 20 25 30 35
E--> 217 Val Phe Val Pro Asn Asn Glu Ala Iso Glu Asn Tyr Iso Arg Glu Lys Lys Ala
218 40 45 50 55
E--> 220 Thr Ser Leu Lys Glu Asp Iso Leu Arg Tyr His Val Val Leu Gly
221 60 65 70
223 Glu Lys Leu Leu Lys Asn Asp Leu His Asn Gly Met His Arg Glu Thr Met
224 75 80 85
227 Leu Gly Phe Ser Tyr Leu Leu Ala Phe Phe Leu Arg Asn Asp Gln Leu Tyr Val Asn
228 90 95 100 105
E--> 230 Glu Ala Pro Iso Asn Tyr Thr Asn Val Ala Thr Asp Lys Gly Val Iso His Gly Leu
231 110 115 120 125
E--> 233 Glu Lys Val Leu Glu Iso Gln Lys Asn Arg Cys Asp Asn Asn Asp Thr Iso Iso Val
234 130 135 140 145
236 Arg Gly Glu Cys Gly Lys Cys Ser Gln Ala Pro Cys Pro Leu Glu Thr Lys Pro
237 150 155 160
E--> 239 Leu Arg Glu Thr Arg Lys Cys Iso Tyr Ser Iso Tyr Phe Met Gly Lys Arg Ser Val
240 165 170 175 180
E--> 243 Phe Iso Gly Cys Gln Pro Gln Cys Val Arg Thr Iso Iso Thr Arg Ala Cys Trp Leu
244 185 190 195 200
246 Ala Ser Leu Ala His Asn Ala Lys Pro Ala Pro Gly Glu Val Lys Met Cys Ala Leu
247 205 210 215 220
249 Gly Thr Ala Ser Val Trp Asp Gly Val Asn Gly Thr Gly Thr Cys Gln Cys Gly Leu
250 225 230 235 240
E--> 252 Gly Phe Asn Gly Thr Ala Cys Glu Thr Cys Thr Glu Gly Lys Tyr Gly Iso His Cys
253 245 250 255
255 Asp Gln Ala Cys Ser Cys Val His Gly Arg Cys Ser Gln Gly Pro Leu Gly Asp Gly

See p. 4
for explanation

<110> Weigel et al.
 <120> Identification of Hyaluronan Receptor for Endocytosis
 <130> 5820.603
 <140> Not Yet Assigned
 <141> Herewith
 <160> 87
 <170> WordPerfect 8.0 *Software*
 <210> 2
 <211> 1431
 <212> PRT
 <213> Rattus norvegicus
 <220>

<225> ~~400~~ HARE protein

<400> 2

Ser Leu Pro Ser Leu Leu Thr Arg Leu Glu Gln Met Pro Asp Tyr Ser Iso Phe Arg
 1 5 10 15
 Gly Tyr Iso Iso His Tyr Asn Leu Ala Ser Ala Iso Glu Ser Ala Asp Ala Tyr Thr
 20 25 30 35

Per 1.822 of sequence rules, a MAXIMUM of 16 amino acids per line allowed.

invalid - use I/e for

Isoleucine

Please consult WIPo Standard ST.25, appendix 2, Tables 1-4, for correct nucleotide and amino acid format.

The above is a sample of global errors. Please edit all amino acid sequences.

delete section

~~<110> Weigel et al.~~
~~<120> Identification of Hyaluronan Receptor for Endocytosis~~
~~<130> 5820.603~~
~~<140> Not Yet Assigned~~
~~<141> Herewith~~
~~<160> 57~~
~~<170> WordPerfect 8.0 *Software*~~
~~<210> 3~~
~~<211> 20~~
~~<212> DNA~~
~~<213> Rattus norvegicus~~
~~<220>~~
 <223> ~~<400>~~ Primer 208F

<400> 3

invalid for use in the sequence

TNTTYGCICC

20

CONTTYACNG

move these onto same line, with cumulative base total figure at right margin of the line

- 1) Use lower-case letters for all bases
- 2) See item 10 on EPO summary sheet regarding use of n's in a sequence, and Xaa's in an amino acid sequence
- 3) See Tables 1 and 2 regarding use of modified or unusual nucleotides (Appendix 2, WIPO Standard ST.25)
- 4) See sample Sequence Listing (attached) for valid format.

<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001

<141> 1998-12-31

<150> US 08/999,999

<151> 1997-10-15

<160> 4

<170> PatentIn version 2.0

<210> 1

<211> 389

<212> DNA

<213> Paramecium sp.

<220>

<221> CDS

<222> (279)...(389)

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a
Protease from Paramecium sp.

<303> Journal of Genes

<304> 1

<305> 4

<306> 1-7

<307> 1988-06-31

<308> 123456

<309> 1988-06-31

<400>	1						
agctgtagtc	attcctgtgt	cctcttctct	ctgggcttct	cacctgcta	atcagatctc		60
agggagagtg	tcttgacct	cctctgcctt	tgcagcttca	caggcaggca	ggcaggcagc		120
tgatgtggca	attgctggca	gtgccacagg	cttttcagcc	aggcttaggg	tgggttcgcg		180
cgcggcgcg	cggccctct	cgcgctctc	tgcgctctc	ctctcgtct	cctctcgtc		240



Appendix 3, page 2

ggacctgatt aggtgagcag gaggaggggg cagttagc atg gtt tca atg ttc agc 296
Met Val Ser Met Phe Ser
1 5

ttg tct ttc aaa tgg cct gga ttt tgt ttg ttt gtt tgt ttg ttc caa 344
Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val Cys Leu Phe Gln
10 15 20

tgt ccc aaa gtc ctc ccc tgt cac tca tca ctg cag ccg aat ctt 389
Cys Pro Lys Val Leu Pro Cys His Ser Ser Leu Gln Pro Asn Leu
25 30 35

<210> 2
<211> 37
<212> PRT
<213> Paramecium sp.

<400> 2
Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu
1 5 10 15

Phe Val Cys Leu Phe Gln Cys Pro Lys Val Leu Pro Cys His Ser Ser
20 25 30

Leu Gln Pro Asn Leu
35

<210> 3
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide based on size and polarity to act as a
linker between the alpha and beta chains of Protein XYZ.

<400> 3
Met Val Asn Leu Glu Pro Met His Thr Glu Ile
1 5 10

<210> 4
<400> 4
000

[Annex VIII follows]



identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

		in feature	base was used in a sequence
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	0
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	0
<302>	Title		0
<303>	Journal		0
<304>	Volume		0
<305>	Issue		0
<306>	Pages		0
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	0
<308>	Database Accession Number	Accession number assigned by database including database name	0
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	0
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	0

<311>	Patent Filing Date	Document filing date, for patent- type citations only; specify as yyyy-mm-dd	O
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	O
<313>	Relevant Residues	FROM (position) TO (position)	O
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line pre- ceding the actual sequence	M

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.821(e) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/842,930

DATE: 05/11/2001

TIME: 15:27:42

Input Set : A:\SEQUENCES.txt

Output Set: N:\CRF3\05112001\I842930.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier
L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:7 M:283 W: Missing Blank Line separator, <140> field identifier
L:7 M:270 C: Current Application Number differs, Replaced Current Application Number
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:11 M:283 W: Missing Blank Line separator, <210> field identifier
L:15 M:283 W: Missing Blank Line separator, <220> field identifier
L:16 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:1 differs:0
L:16 M:283 W: Missing Blank Line separator, <400> field identifier
L:19 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=1
L:79 M:254 E: No. of Bases conflict, LENGTH:Input:1820 Counted:1860 SEQ:1
L:195 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:195 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:196 M:283 W: Missing Blank Line separator, <120> field identifier
L:196 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:196 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:197 M:283 W: Missing Blank Line separator, <130> field identifier
L:197 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:197 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:198 M:283 W: Missing Blank Line separator, <140> field identifier
L:198 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:198 M:270 C: Current Application Number differs, Replaced Current Application Number
L:199 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:199 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
L:199 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:200 M:283 W: Missing Blank Line separator, <160> field identifier
L:200 M:280 W: Numeric Identifier already exists, <160> found multiple times
L:200 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
L:201 M:280 W: Numeric Identifier already exists, <170> found multiple times
L:202 M:283 W: Missing Blank Line separator, <210> field identifier
L:206 M:283 W: Missing Blank Line separator, <220> field identifier
L:207 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:0
L:207 M:283 W: Missing Blank Line separator, <400> field identifier
L:211 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:214 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:217 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:220 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:230 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:233 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:239 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:243 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:252 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:258 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:267 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:270 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:273 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/842,930

DATE: 05/11/2001

TIME: 15:27:42

Input Set : A:\SEQUENCES.txt

Output Set: N:\CRF3\05112001\I842930.raw

L:279 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:282 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:285 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:294 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:300 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:303 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:306 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:312 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:321 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:324 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:327 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:330 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:333 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:336 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:339 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:346 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
 M:332 Repeated in SeqNo=2
 L:354 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:360 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:369 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:384 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:393 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:405 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:408 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:414 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:417 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
 L:420 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:423 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:429 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:435 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:485 M:280 W: Numeric Identifier already exists, <110> found multiple times
 L:485 M:281 W: Numeric Fields not Ordered, <110> not ordered!
 L:486 M:283 W: Missing Blank Line separator, <120> field identifier
 L:486 M:280 W: Numeric Identifier already exists, <120> found multiple times
 L:486 M:281 W: Numeric Fields not Ordered, <120> not ordered!
 L:487 M:283 W: Missing Blank Line separator, <130> field identifier
 L:487 M:280 W: Numeric Identifier already exists, <130> found multiple times
 L:487 M:281 W: Numeric Fields not Ordered, <130> not ordered!
 L:488 M:283 W: Missing Blank Line separator, <140> field identifier
 L:488 M:281 W: Numeric Fields not Ordered, <140> not ordered!
 L:488 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:489 M:280 W: Numeric Identifier already exists, <141> found multiple times
 L:489 M:281 W: Numeric Fields not Ordered, <141> not ordered!
 L:489 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:490 M:283 W: Missing Blank Line separator, <160> field identifier
 L:490 M:280 W: Numeric Identifier already exists, <160> found multiple times
 L:490 M:281 W: Numeric Fields not Ordered, <160> not ordered!
 L:491 M:280 W: Numeric Identifier already exists, <170> found multiple times
 L:492 M:283 W: Missing Blank Line separator, <210> field identifier

VERIFICATION SUMMARY

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Input Set : A:\SEQUENCES.txt

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L:496 M:283 W: Missing Blank Line separator, <220> field identifier
L:497 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:0
L:497 M:283 W: Missing Blank Line separator, <400> field identifier
L:500 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:0
L:500 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:0
L:500 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:0
L:500 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:500 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:500 M:112 C: (48) String data converted to lower case,
L:534 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:534 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:535 M:283 W: Missing Blank Line separator, <120> field identifier
L:535 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:535 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:536 M:283 W: Missing Blank Line separator, <130> field identifier
L:536 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:536 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:537 M:283 W: Missing Blank Line separator, <140> field identifier
L:537 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:537 M:270 C: Current Application Number differs, Replaced Current Application Number
L:538 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:538 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
L:538 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:539 M:283 W: Missing Blank Line separator, <160> field identifier
L:539 M:280 W: Numeric Identifier already exists, <160> found multiple times
L:539 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
L:540 M:280 W: Numeric Identifier already exists, <170> found multiple times
L:541 M:283 W: Missing Blank Line separator, <210> field identifier
L:545 M:283 W: Missing Blank Line separator, <220> field identifier
L:546 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:4 differs:0
L:546 M:283 W: Missing Blank Line separator, <400> field identifier
L:549 M:112 C: (48) String data converted to lower case,
L:583 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:583 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:584 M:283 W: Missing Blank Line separator, <120> field identifier
L:584 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:584 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:585 M:283 W: Missing Blank Line separator, <130> field identifier
L:585 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:585 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:586 M:283 W: Missing Blank Line separator, <140> field identifier
L:586 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:586 M:270 C: Current Application Number differs, Replaced Current Application Number
L:587 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:587 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
L:587 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:588 M:283 W: Missing Blank Line separator, <160> field identifier
L:588 M:280 W: Numeric Identifier already exists, <160> found multiple times
L:588 M:281 W: Numeric Fields not Ordered, <160> not ordered!.

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Input Set : A:\SEQUENCES.txt

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L:589 M:280 W: Numeric Identifier already exists, <170> found multiple times
 L:590 M:283 W: Missing Blank Line separator, <210> field identifier
 L:594 M:283 W: Missing Blank Line separator, <220> field identifier
 L:595 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:5 differs:0
 L:595 M:283 W: Missing Blank Line separator, <400> field identifier
 L:599 M:112 C: (48) String data converted to lower case,
 L:632 M:280 W: Numeric Identifier already exists, <110> found multiple times
 L:632 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
 L:633 M:283 W: Missing Blank Line separator, <120> field identifier
 L:633 M:280 W: Numeric Identifier already exists, <120> found multiple times
 L:633 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
 L:634 M:283 W: Missing Blank Line separator, <130> field identifier
 L:634 M:280 W: Numeric Identifier already exists, <130> found multiple times
 L:634 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
 L:635 M:283 W: Missing Blank Line separator, <140> field identifier
 L:635 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
 L:635 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:636 M:280 W: Numeric Identifier already exists, <141> found multiple times
 L:636 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
 L:636 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:637 M:283 W: Missing Blank Line separator, <160> field identifier
 L:637 M:280 W: Numeric Identifier already exists, <160> found multiple times
 L:637 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
 L:638 M:280 W: Numeric Identifier already exists, <170> found multiple times
 L:639 M:283 W: Missing Blank Line separator, <210> field identifier
 L:643 M:283 W: Missing Blank Line separator, <220> field identifier
 L:644 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:6 differs:0
 L:644 M:283 W: Missing Blank Line separator, <400> field identifier
 L:647 M:112 C: (48) String data converted to lower case,
 L:681 M:280 W: Numeric Identifier already exists, <110> found multiple times
 L:681 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
 L:682 M:283 W: Missing Blank Line separator, <120> field identifier
 L:682 M:280 W: Numeric Identifier already exists, <120> found multiple times
 L:682 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
 L:683 M:283 W: Missing Blank Line separator, <130> field identifier
 L:683 M:280 W: Numeric Identifier already exists, <130> found multiple times
 L:683 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
 L:684 M:283 W: Missing Blank Line separator, <140> field identifier
 L:684 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
 L:684 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:685 M:280 W: Numeric Identifier already exists, <141> found multiple times
 L:685 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
 L:685 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:686 M:283 W: Missing Blank Line separator, <160> field identifier
 L:686 M:280 W: Numeric Identifier already exists, <160> found multiple times
 L:686 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
 L:687 M:280 W: Numeric Identifier already exists, <170> found multiple times
 L:688 M:283 W: Missing Blank Line separator, <210> field identifier
 L:692 M:283 W: Missing Blank Line separator, <220> field identifier

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Input Set : A:\SEQUENCES.txt

Output Set: N:\CRF3\05112001\I842930.raw

L:693 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:7 differs:0
 L:693 M:283 W: Missing Blank Line separator, <400> field identifier
 L:696 M:112 C: (48) String data converted to lower case,
 L:730 M:280 W: Numeric Identifier already exists, <110> found multiple times
 L:730 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
 L:731 M:283 W: Missing Blank Line separator, <120> field identifier
 L:731 M:280 W: Numeric Identifier already exists, <120> found multiple times
 L:731 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
 L:732 M:280 W: Numeric Identifier already exists, <130> found multiple times
 L:732 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
 L:733 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
 L:733 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:734 M:280 W: Numeric Identifier already exists, <141> found multiple times
 L:734 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
 L:734 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:735 M:280 W: Numeric Identifier already exists, <160> found multiple times
 L:735 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
 L:736 M:280 W: Numeric Identifier already exists, <170> found multiple times
 L:742 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:8 differs:0
 L:779 M:280 W: Numeric Identifier already exists, <110> found multiple times
 L:779 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
 L:780 M:280 W: Numeric Identifier already exists, <120> found multiple times
 L:780 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
 L:781 M:280 W: Numeric Identifier already exists, <130> found multiple times
 L:781 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
 L:782 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
 L:782 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:783 M:280 W: Numeric Identifier already exists, <141> found multiple times
 L:783 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
 L:783 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:784 M:280 W: Numeric Identifier already exists, <160> found multiple times
 L:784 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
 L:785 M:280 W: Numeric Identifier already exists, <170> found multiple times
 L:791 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:9 differs:0
 L:828 M:280 W: Numeric Identifier already exists, <110> found multiple times
 L:828 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
 L:829 M:280 W: Numeric Identifier already exists, <120> found multiple times
 L:829 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
 L:831 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:832 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:840 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:10 differs:0
 L:880 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:881 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:889 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:11 differs:0
 L:892 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:929 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:930 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:938 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:12 differs:0
 L:978 M:270 C: Current Application Number differs, Replaced Current Application Number

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L:979 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:987 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:13 differs:0
L:990 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1027 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1028 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1036 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:14 differs:0
L:1039 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1076 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1077 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1085 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:15 differs:0
L:1125 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1126 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1134 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:16 differs:0
L:1137 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:0
L:1137 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:0
L:1137 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:0
L:1137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1137 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1137 M:112 C: (48) String data converted to lower case,
L:1174 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1175 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1183 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:17 differs:0
L:1186 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:0
L:1186 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:0
L:1186 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:0
L:1186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1186 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1186 M:112 C: (48) String data converted to lower case,
L:1223 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1224 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1232 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:18 differs:0
L:1235 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:0
L:1235 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:0
L:1235 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:0
L:1235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1235 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1235 M:112 C: (48) String data converted to lower case,
L:1272 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1273 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1281 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:19 differs:0
L:1285 M:112 C: (48) String data converted to lower case,
L:1321 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1322 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1330 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:20 differs:0
L:1334 M:112 C: (48) String data converted to lower case,
L:1370 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1371 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:1379 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:21 differs:0
L:1383 M:112 C: (48) String data converted to lower case,

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L:1419 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:1420 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:1428 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:22 differs:0
 L:1431 M:112 C: (48) String data converted to lower case,
 L:1468 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:1469 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:1477 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:23 differs:0
 L:1480 M:112 C: (48) String data converted to lower case,
 L:1517 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:1518 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:1526 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:24 differs:0
 L:1529 M:112 C: (48) String data converted to lower case,
 M:112 Repeated in SeqNo=24
 L:1614 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:1615 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:1623 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:25 differs:0
 L:1627 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:1630 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:1838 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
 M:332 Repeated in SeqNo=25
 L:1860 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:1861 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:1869 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:26 differs:0
 L:1872 M:112 C: (48) String data converted to lower case,
 L:1909 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:1910 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:1918 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:27 differs:0
 L:1958 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:1959 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:1967 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:28 differs:0
 L:2007 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:2008 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:2016 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:29 differs:0
 L:2019 M:112 C: (48) String data converted to lower case,
 L:2056 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:2057 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:2065 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:30 differs:0
 L:2068 M:112 C: (48) String data converted to lower case,
 L:2105 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:2106 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:2114 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:31 differs:0
 L:2117 M:112 C: (48) String data converted to lower case,
 L:2154 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:2155 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:2163 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:32 differs:0
 L:2166 M:112 C: (48) String data converted to lower case,
 L:2203 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:2204 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:2212 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:33 differs:0

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L:2215 M:112 C: (48) String data converted to lower case,
L:2252 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2253 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2261 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:34 differs:0
L:2264 M:112 C: (48) String data converted to lower case,
L:2301 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2302 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2310 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:35 differs:0
L:2313 M:112 C: (48) String data converted to lower case,
L:2350 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2351 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2359 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:36 differs:0
L:2362 M:112 C: (48) String data converted to lower case,
L:2399 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2400 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2403 M:214 E: (33) Seq.# missing, SEQ ID NO:37
L:2408 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:38 differs:0
L:2411 M:112 C: (48) String data converted to lower case,
L:2448 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2449 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2457 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:39 differs:0
L:2460 M:112 C: (48) String data converted to lower case,
L:2497 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2498 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2506 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:40 differs:0
L:2509 M:112 C: (48) String data converted to lower case,
L:2546 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2547 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2555 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:41 differs:0
L:2595 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2596 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2604 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:42 differs:0
L:2644 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2645 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2653 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:43 differs:0
L:2693 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2694 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2702 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:44 differs:0
L:2742 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2743 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2751 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:45 differs:0
L:2791 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2792 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2800 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:46 differs:0
L:2840 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2841 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:2849 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:47 differs:0
L:2889 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2890 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/842,930

DATE: 05/11/2001

TIME: 15:27:43

Input Set : A:\SEQUENCES.txt

Output Set: N:\CRF3\05112001\I842930.raw

L:2898 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:48 differs:0
 L:2938 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:2939 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:2947 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:49 differs:0
 L:2987 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:2988 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:2996 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:50 differs:0
 L:3036 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:3037 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:3045 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:51 differs:0
 L:3086 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
 L:3332 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (57) Counted (56)